



SEQUENCE LISTING

<10> Max-Planck-Gesellschaft z.  
Förd. d. Wissenschaften

<120> Plants With Modified Gene Expression

<130> DEBE:005US

<140> 10/030,386

<140> 2002-01-02

<150> PCT/DE00/02233

<151> 2000-07-03

<150> DE 199 30 570.6

<151> 1999-07-02

<160> 8

<170> PatentIn Ver. 2.1

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<211> 3389

<212> DNA

<213> *Arabidopsis thaliana*

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<212> PRT  
<213> *Arabidopsis thaliana*

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Gln Asn Ser Cys Ile Asn Asn Thr Leu Ile Glu Pro Leu Pro Leu Ile  
35 40 45  
  
Asp Arg Ile Asn Leu Asn Ser Asn Leu Asp Leu Asn Pro Asn Pro Leu  
50 55 60  
  
Tyr Ala Glu Glu Gly Glu Gln Glu Glu Glu Glu Glu Glu Glu Asp  
65 70 75 80  
  
Arg Glu Val Asp Val Asp Leu His Ile Gly Leu Pro Gly Phe Gly Lys  
85 90 95  
  
Pro Ser Asn Asp Ala Lys Gln Leu Lys Lys Arg Asn Gly Lys Glu Ile  
100 105 110  
  
Ala Thr Tyr Asp Ala Gly Lys Gly Ile Glu Asn Glu Leu Ser Gly Lys  
115 120 125  
  
Ala Tyr Trp Ile Pro Ala Pro Glu Gln Ile Leu Ile Gly Phe Thr His  
130 135 140  
  
Phe Ser Cys His Val Cys Phe Lys Thr Phe Asn Arg Tyr Asn Asn Leu  
145 150 155 160  
  
Gln Met His Met Trp Gly His Gly Ser Gln Tyr Arg Lys Gly Pro Glu  
165 170 175  
  
Ser Leu Lys Gly Thr Gln Pro Arg Ala Met Leu Gly Ile Pro Cys Tyr  
180 185 190  
  
Cys Cys Val Glu Gly Cys Arg Asn His Ile Asp His Pro Arg Ser Lys  
195 200 205  
  
Pro Leu Lys Asp Phe Arg Thr Leu Gln Thr His Tyr Lys Arg Lys His  
210 215 220  
  
Gly His Lys Pro Phe Ser Cys Arg Leu Cys Gly Lys Leu Leu Ala Val  
225 230 235 240  
  
Lys Gly Asp Trp Arg Thr His Glu Lys Asn Cys Gly Lys Arg Trp Val  
245 250 255

Cys Val Cys Gly Ser Asp Phe Lys His Lys Arg Ser Leu Lys Asp His  
260 265 270

Val Lys Ala Phe Gly Ser Gly His Gly Pro Tyr Pro Thr Gly Leu Phe  
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290 295 300

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<211> 1816

<212> DNA

<213> *Arabidopsis thaliana*

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<211> 383

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

Peptide

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20 25 30

Leu Pro Pro Val Thr Pro Pro Ser Ser Phe Phe Phe Pro Gln Ser  
35 40 45

Gly Asp Leu Arg Arg Pro Pro Pro Pro Thr Pro Pro Pro Ser Pro  
50 55 60

Pro Leu Arg Glu Ala Leu Pro Leu Leu Ser Leu Ser Pro Ala Asn Lys  
65 70 75 80

Gln Gln Asp His His Asn His Asp His Leu Ile Gln Glu Pro Pro  
85 90 95

Ser Thr Ser Met Asp Val Asp Tyr Asp His His His Gln Asp Asp His  
100 105 110

His Asn Leu Asp Asp Asp Asp His Asp Val Thr Val Ala Leu His Ile  
115 120 125

Gly Leu Pro Ser Pro Ser Ala Gln Glu Met Ala Ser Leu Leu Met Met  
130 135 140

Ser Ser Ser Ser Ser Arg Thr Thr His His His Glu Asp Met  
145 150 155 160

Asn His Lys Lys Asp Leu Asp His Glu Tyr Ser His Gly Ala Val Gly  
165 170 175

Gly Gly Glu Asp Asp Glu Asp Ser Val Gly Gly Asp Gly Gly Cys  
180 185 190

Arg Ile Ser Arg Leu Asn Lys Gly Gln Tyr Trp Ile Pro Thr Pro Ser  
195 200 205

Gln Ile Leu Ile Gly Pro Thr Gln Phe Ser Cys Pro Val Cys Phe Lys  
210 215 220

Thr Phe Asn Arg Tyr Asn Asn Met Gln Met His Met Trp Gly His Gly  
225 230 235 240

Ser Gln Tyr Arg Lys Gly Pro Glu Ser Leu Arg Gly Thr Gln Pro Thr  
245 250 255

Gly Met Leu Arg Leu Pro Cys Tyr Cys Cys Ala Pro Gly Cys Arg Asn  
260 265 270

Asn Ile Asp His Pro Arg Ala Lys Pro Leu Lys Asp Phe Arg Thr Leu

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Lys Cys Gly Lys Ala Phe Ala Val Arg Gly Asp Trp Arg Thr His Glu		
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Lys Asn Cys Gly Lys Leu Trp Tyr Cys Ile Cys Gly Ser Asp Phe Lys		
325	330	335
His Lys Arg Ser Leu Lys Asp His Ile Lys Ala Phe Gly Asn Gly His		
340	345	350
Gly Ala Tyr Gly Ile Asp Gly Phe Asp Glu Glu Asp Glu Pro Ala Ser		
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Glu Val Glu Gln Leu Asp Asn Asp His Glu Ser Met Gln Ser Lys		
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Tyr Leu Ala Phe Thr Gly Phe Leu Thr Gln Leu His His Leu Glu Ile		
35	40	45
Ser Cys Leu Leu Leu Phe Phe Ser Leu Ser Ser Leu Leu Lys Leu		
50	55	60
Met Ala Asp Pro Asp Cys Ile Phe Arg Asn Gly Tyr Val Asp Tyr Tyr		
65	70	75
80		
Asn Tyr Ser Phe Asn Tyr Ala Thr Ser Leu Ser Arg Ile Tyr Asn Ser		
85	90	95
His Asp Ser Phe Phe Phe Pro Gln Ser Gly Asp Leu Arg Arg Pro		
100	105	110
Pro Pro Pro Pro Thr Pro Pro Ser Pro Pro Leu Arg Glu Ala Leu		
115	120	125

Pro Leu Leu Ser Leu Ser Pro Ala Asn Thr Gln Gln Asp His His His  
130 135 140

Asn His Asp His Leu Ile Gln Glu Pro Pro Ser Thr Ser Met Asp Val  
145 150 155 160

Asp Tyr Asp His His His Gln Asp Asp His His Asn Leu Asp Asp Asp  
165 170 175

Asp His Asp Val Thr Val Ala Leu His Ile Gly Leu Pro Ser Pro Ser  
180 185 190

Ala Gln Glu Met Ala Ser Leu Leu Met Met Ser Ser Ser Ser Ser Ser  
195 200 205

Ser Arg Thr Thr His His His Glu Asp Met Asn His Lys Lys Asp Leu  
210 215 220

Asp His Glu Tyr Ser His Gly Ala Val Gly Gly Glu Asp Asp Asp  
225 230 235 240

Glu Asp Ser Val Gly Gly Asp Gly Gly Cys Arg Ile Ser Arg Leu Asn  
245 250 255

Lys Gly Gln Tyr Trp Ile Pro Thr Pro Ser Gln Ile Leu Ile Gly Pro  
260 265 270

Thr Gln Phe Ser Cys Pro Val Cys Phe Lys Thr Phe Asn Arg Tyr Asn  
275 280 285

Asn Met Gln Met His Met Trp Gly His Gly Ser Gln Tyr Arg Lys Gly  
290 295 300

Pro Glu Ser Leu Arg Gly Thr Gln Pro Thr Gly Met Leu Arg Leu Pro  
305 310 315 320

Cys Tyr Cys Cys Ala Pro Gly Cys Arg Asn Asn Ile Asp His Pro Arg  
325 330 335

Ala Lys Pro Leu Lys Asp Phe Arg Thr Leu Gln Thr His Tyr Lys Arg  
340 345 350

Lys His Gly Ile Lys Pro Phe Met Cys Arg Lys Cys Gly Lys Ala Phe  
355 360 365

Ala Val Arg Gly Asp Trp Arg Thr His Glu Lys Asn Cys Gly Lys Leu  
370 375 380

Trp Tyr Cys Ile Cys Gly Ser Asp Phe Lys His Lys Arg Ser Leu Lys  
385 390 395 400

Asp His Ile Lys Ala Phe Thr Asn Gly His Gly Ala Tyr Gly Ile Asp  
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Gly Phe Asp Glu Glu Asp Glu Pro Ala Ser Glu Val Glu Gln Leu Asp

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425

430

Asn Asp His Glu Ser Met Gln Ser Lys  
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<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Peptide

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Gly Ser Tyr Tyr Tyr Ser Asn Thr Thr Asn Pro Asn Tyr Ile Asn His  
35 40 45

Thr His Thr Thr Ser Thr Ser Pro Asn Ser Pro Pro Leu Arg Glu Ala  
50 55 60

Leu Pro Leu Leu Ser Leu Ser Pro Ile Arg His Gln Glu Gln Gln Asp  
65 70 75 80

Gln His Tyr Phe Met Asp Thr His Gln Ile Ser Ser Ser Asn Phe Leu  
85 90 95

Asp Asp Pro Leu Val Thr Val Asp Leu His Leu Gly Leu Pro Asn Tyr  
100 105 110

Gly Val Gly Glu Ser Ile Arg Ser Asn Ile Ala Pro Asp Ala Thr Thr  
115 120 125

Asp Glu Gln Asp Gln Asp His Asp Arg Gly Val Glu Val Thr Val Glu  
130 135 140

Ser His Leu Asp Asp Asp Asp His His Gly Asp Leu His Arg Gly  
145 150 155 160

His His Tyr Trp Ile Pro Thr Pro Ser Gln Ile Leu Ile Gly Pro Thr  
165 170 175

Gln Phe Thr Cys Pro Leu Cys Phe Lys Thr Phe Asn Arg Tyr Asn Asn  
180 185 190

Met Gln Asn Asn Ile Asp His Pro Arg Ala Lys Pro Leu Lys Asp Phe  
195 200 205

Arg Thr Leu Gln Thr His Tyr Lys Arg Lys His Gly Ser Lys Pro Phe  
210 215 220

Ala Cys Arg Met Cys Gly Lys Ala Phe Ala Val Lys Gly Asp Trp Arg  
225 230 235 240

Thr His Glu Lys Asn Cys Gly Lys Leu Trp Tyr Cys Ser Cys Gly Ser  
245 250 255

Asp Phe Lys His Lys Arg Ser Leu Lys Asp His Val Lys Ala Phe Gly  
260 265 270

Asn Gly His Val Pro Cys Gly Ile Asp Ser Phe Gly Gly Asp His Glu  
275 280 285

Asp Tyr Tyr Asp Ala Ala Ser Asp Ile Glu Gln  
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<210> 8

<211> 54

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Peptide

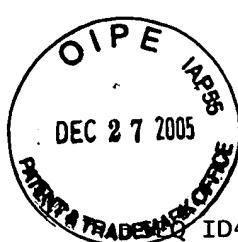
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Gln Met His Met Trp Gly His Gly Arg Glu Tyr Arg Lys Gly Pro Glu  
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Ser Leu Lys Gly Thr Gln Thr Val Ala Leu Leu Lys Val Pro Cys Tyr  
20 25 30

Cys Ala Ala Gly Cys Arg Asn Ser Val Ser His Pro Arg Ala Arg Pro  
35 40 45

Leu Lys Asp Phe Arg Thr  
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## SEQ2-4align\_051124MS.txt

ID4 (TT1 genomic DNA, lower case) vs. SEQ ID2 (TT1 CDS, upper case)



## SEQ2-4align\_051124MS.txt

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786	TTTTAACACAAACGTTCTCTTAAGGACCATGTTAAGGCCTTGGGCTG	835
1461	gtcatgggccttatccaactggttgttgaagagcaggcttctaattca	1510
836	GTCATGGGCCTTATCCAACACTGGTTGAAGAGCAGGCTTCTAATTCA	885
1511	tctgtctccgagacttggggggaaatttg.....agctt	1816
886	TCTGTCTCCGAGACTTGTGGGGAA	912

Note Best alignment is between forward est and forward genome, and splice sites imply forward gene

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+Intron	-20	0.0	484	1108		
Exon	429	100.0	1109	1537	484	912
Span	892	100.0	1	1537	1	912
Segment	483	100.0	1	483	1	483
Segment	429	100.0	1109	1537	484	912

Alignment Score: 892